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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/919,935

DATE: 11/13/2001

TIME: 14:04:28

Input Set : A:\211712US0X.txt

Output Set: N:\CRF3\11132001\I919935.raw

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3 <110> APPLICANT: BATHE, BRIGITTE
4     MOCKEL, BETTINA
5     PFEFFERLE, WALTER
6     HUTHMACHER, KLAUS
7     BINDER, MICHAEL
8     GREISSINGER, DIETER
9     THIERBACH, GEORG
11 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES WHICH CODE FOR THE METF GENE
13 <130> FILE REFERENCE: 211712US0X
15 <140> CURRENT APPLICATION NUMBER: 09/919,935
16 <141> CURRENT FILING DATE: 2001-08-02
18 <150> PRIOR APPLICATION NUMBER: DE 10053942.4
19 <151> PRIOR FILING DATE: 2000-08-02
21 <150> PRIOR APPLICATION NUMBER: DE 10109686.0
22 <151> PRIOR FILING DATE: 2001-02-28
24 <150> PRIOR APPLICATION NUMBER: US 60/294,279
25 <151> PRIOR FILING DATE: 2001-05-31
27 <160> NUMBER OF SEQ ID NOS: 4
29 <170> SOFTWARE: PatentIn version 3.1
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32 <211> LENGTH: 1551
33 <212> TYPE: DNA
34 <213> ORGANISM: Corynebacterium glutamicum
36 <220> FEATURE:
37 <221> NAME/KEY: CDS
38 <222> LOCATION: (299)..(1345)
39 <223> OTHER INFORMATION:
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45 ccagcccacg cataaagagg acggattcgc tttcctccat tgagcacgaa actgcgaaga      120
47 tggggccacag catctgtgac aggagcgccg atatcagcaa ttgttagctc ttgagcatcg      180
49 aggaactgcg tcaaacgata tcgcacgacc tccggaaatt tgtcgaggtc aaggatcatgg      240
51 gcatcgaaac tgctcaagga gacgtccttc aatcgaatag ggggatgcgg gctgaatt      298
53 ttg gtg gag gtg aat aaa tgc cag agg cag tcc caa caa aac act ctc      346
54 Leu Val Glu Val Asn Lys Cys Gln Arg Gln Ser Gln Gln Asn Thr Leu
55 1          5          10          15
57 atc aca cta aga tac cca ggc atg tcc cta acg aac atc cca gcc tca      394
58 Ile Thr Leu Arg Tyr Pro Gly Met Ser Leu Thr Asn Ile Pro Ala Ser
59          20          25          30
61 tct caa tgg gca att agc gac gtt ttg aag cgt cct tca ccc ggc cga      442
62 Ser Gln Trp Ala Ile Ser Asp Val Leu Lys Arg Pro Ser Pro Gly Arg
63          35          40          45
65 gta cct ttt tct gtc gag ttt atg cca ccc cgc gac gat gca gct gaa      490
66 Val Pro Phe Ser Val Glu Phe Met Pro Pro Arg Asp Asp Ala Ala Glu
67          50          55          60
69 gag cgt ctt tac cgc gca gca gag gtc ttc cat gac ctc ggt gca tcg      538
70 Glu Arg Leu Tyr Arg Ala Ala Glu Val Phe His Asp Leu Gly Ala Ser

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71	65	70	75	80	
73	ttt gtc tcc gtg act tat ggt gct ggc gga tca acc cgt gag aga acc	586			
74	Phe Val Ser Val Thr Tyr Gly Ala Gly Gly Ser Thr Arg Glu Arg Thr				
75	85 90 95				
77	tca cgt att gct cga cga tta gcg aaa caa ccg ttg acc act ctg gtg	634			
78	Ser Arg Ile Ala Arg Arg Leu Ala Lys Gln Pro Leu Thr Thr Leu Val				
79	100 105 110				
81	cac ctg acc ctg gtt aac cac act cgc gaa gag atg aag gca att ctt	682			
82	His Leu Thr Leu Val Asn His Thr Arg Glu Glu Met Lys Ala Ile Leu				
83	115 120 125				
85	cgg gaa tac cta gag ctg gga tta aca aac ctg ttg gcg ctt cga gga	730			
86	Arg Glu Tyr Leu Glu Leu Gly Leu Thr Asn Leu Leu Ala Leu Arg Gly				
87	130 135 140				
89	gat ccg cct gga gac cca tta ggc gat tgg gtg agc acc gat gga gga	778			
90	Asp Pro Pro Gly Asp Pro Leu Gly Asp Trp Val Ser Thr Asp Gly Gly				
91	145 150 155 160				
93	ctg aac tat gcc tct gag ctg atc gat ctt att aag tcc act cct gag	826			
94	Leu Asn Tyr Ala Ser Glu Leu Ile Asp Leu Ile Lys Ser Thr Pro Glu				
95	165 170 175				
97	ttc cgg gaa ttc gac ctg ggt atc gcc tcc ttc ccc gaa ggg cat ttc	874			
98	Phe Arg Glu Phe Asp Leu Gly Ile Ala Ser Phe Pro Glu Gly His Phe				
99	180 185 190				
101	cgg gcg aaa act cta gaa gaa gac acc aaa tac act ctg gcg aag ctg	922			
102	Arg Ala Lys Thr Leu Glu Glu Asp Thr Lys Tyr Thr Leu Ala Lys Leu				
103	195 200 205				
105	cgt gga ggg gca gag tac tcc atc acg cag atg ttc ttt gat gtg gaa	970			
106	Arg Gly Gly Ala Glu Tyr Ser Ile Thr Gln Met Phe Phe Asp Val Glu				
107	210 215 220				
109	gac tac ctg cga ctt cgt gat cgc ctt gtc gct gca gac ccc att cat	1018			
110	Asp Tyr Leu Arg Leu Arg Asp Arg Leu Val Ala Ala Asp Pro Ile His				
111	225 230 235 240				
113	ggt gcg aag cca atc att cct ggc atc atg ccc att acc gag ctg cgg	1066			
114	Gly Ala Lys Pro Ile Ile Pro Gly Ile Met Pro Ile Thr Glu Leu Arg				
115	245 250 255				
117	tct gtg cgt cga cag gtc gaa ctg tct ggt gct caa ttg ccg agc caa	1114			
118	Ser Val Arg Arg Gln Val Glu Leu Ser Gly Ala Gln Leu Pro Ser Gln				
119	260 265 270				
121	cta gaa gaa tca ctt gtt cga gct gca aac ggc aat gaa gaa gcg aac	1162			
122	Leu Glu Glu Ser Leu Val Arg Ala Ala Asn Gly Asn Glu Glu Ala Asn				
123	275 280 285				
125	aaa gac gag atc cgc aag gtg ggc att gaa tat tcc acc aat atg gca	1210			
126	Lys Asp Glu Ile Arg Lys Val Gly Ile Glu Tyr Ser Thr Asn Met Ala				
127	290 295 300				
129	gag cga ctg att gcc gaa ggt gcg gaa gat ctg cac ttc atg acg ctt	1258			
130	Glu Arg Leu Ile Ala Glu Gly Ala Glu Asp Leu His Phe Met Thr Leu				
131	305 310 315 320				
133	aac ttc acc cgt gca acc caa gaa gtg ttg tac aac ctt ggc atg gcg	1306			
134	Asn Phe Thr Arg Ala Thr Gln Glu Val Leu Tyr Asn Leu Gly Met Ala				
135	325 330 335				

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137 cct gct tgg gga gca gag cac ggc caa gac gcg gtg cgt taagccctct 1355
138 Pro Ala Trp Gly Ala Glu His Gly Gln Asp Ala Val Arg
139          340          345
141 taggaatcat gaaggggggag ggcggtgac aatacggcaa acggccggttg atccccgtca 1415
143 aacctaaact gcctgagcaa gtcagtgaag ccgagagagc gatacaggct aaacgcattg 1475
145 ttgcctcat cgtcgacctc ggggtgtagac aaaatggcaa aagtgttttg tttgtctttt 1535
147 aacagttcat gcatca 1551
150 <210> SEQ ID NO: 2
151 <211> LENGTH: 349
152 <212> TYPE: PRT
153 <213> ORGANISM: Corynebacterium glutamicum
155 <400> SEQUENCE: 2
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158 1          5          10          15
161 Ile Thr Leu Arg Tyr Pro Gly Met Ser Leu Thr Asn Ile Pro Ala Ser
162          20          25          30
165 Ser Gln Trp Ala Ile Ser Asp Val Leu Lys Arg Pro Ser Pro Gly Arg
166          35          40          45
169 Val Pro Phe Ser Val Glu Phe Met Pro Pro Arg Asp Asp Ala Ala Glu
170          50          55          60
173 Glu Arg Leu Tyr Arg Ala Ala Glu Val Phe His Asp Leu Gly Ala Ser
174 65          70          75          80
177 Phe Val Ser Val Thr Tyr Gly Ala Gly Gly Ser Thr Arg Glu Arg Thr
178          85          90          95
181 Ser Arg Ile Ala Arg Arg Leu Ala Lys Gln Pro Leu Thr Thr Leu Val
182          100          105          110
185 His Leu Thr Leu Val Asn His Thr Arg Glu Glu Met Lys Ala Ile Leu
186          115          120          125
189 Arg Glu Tyr Leu Glu Leu Gly Leu Thr Asn Leu Leu Ala Leu Arg Gly
190          130          135          140
193 Asp Pro Pro Gly Asp Pro Leu Gly Asp Trp Val Ser Thr Asp Gly Gly
194 145          150          155          160
197 Leu Asn Tyr Ala Ser Glu Leu Ile Asp Leu Ile Lys Ser Thr Pro Glu
198          165          170          175
201 Phe Arg Glu Phe Asp Leu Gly Ile Ala Ser Phe Pro Glu Gly His Phe
202          180          185          190
205 Arg Ala Lys Thr Leu Glu Glu Asp Thr Lys Tyr Thr Leu Ala Lys Leu
206          195          200          205
209 Arg Gly Gly Ala Glu Tyr Ser Ile Thr Gln Met Phe Phe Asp Val Glu
210          210          215          220
213 Asp Tyr Leu Arg Leu Arg Asp Arg Leu Val Ala Ala Asp Pro Ile His
214 225          230          235          240
217 Gly Ala Lys Pro Ile Ile Pro Gly Ile Met Pro Ile Thr Glu Leu Arg
218          245          250          255
221 Ser Val Arg Arg Gln Val Glu Leu Ser Gly Ala Gln Leu Pro Ser Gln
222          260          265          270
225 Leu Glu Glu Ser Leu Val Arg Ala Ala Asn Gly Asn Glu Glu Ala Asn
226          275          280          285
229 Lys Asp Glu Ile Arg Lys Val Gly Ile Glu Tyr Ser Thr Asn Met Ala

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230      290      295      300
233 Glu Arg Leu Ile Ala Glu Gly Ala Glu Asp Leu His Phe Met Thr Leu
234 305      310      315      320
237 Asn Phe Thr Arg Ala Thr Gln Glu Val Leu Tyr Asn Leu Gly Met Ala
238      325      330      335
241 Pro Ala Trp Gly Ala Glu His Gly Gln Asp Ala Val Arg
242      340      345
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246 <211> LENGTH: 46
247 <212> TYPE: DNA
248 <213> ORGANISM: Artificial sequence
250 <220> FEATURE:
251 <223> OTHER INFORMATION: Synthetic DNA
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259 <212> TYPE: DNA
260 <213> ORGANISM: Artificial sequence
262 <220> FEATURE:
263 <223> OTHER INFORMATION: Synthetic DNA
265 <400> SEQUENCE: 4
266 gatctactcg agttcttcta gttggctcgg      30

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VERIFICATION SUMMARY

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